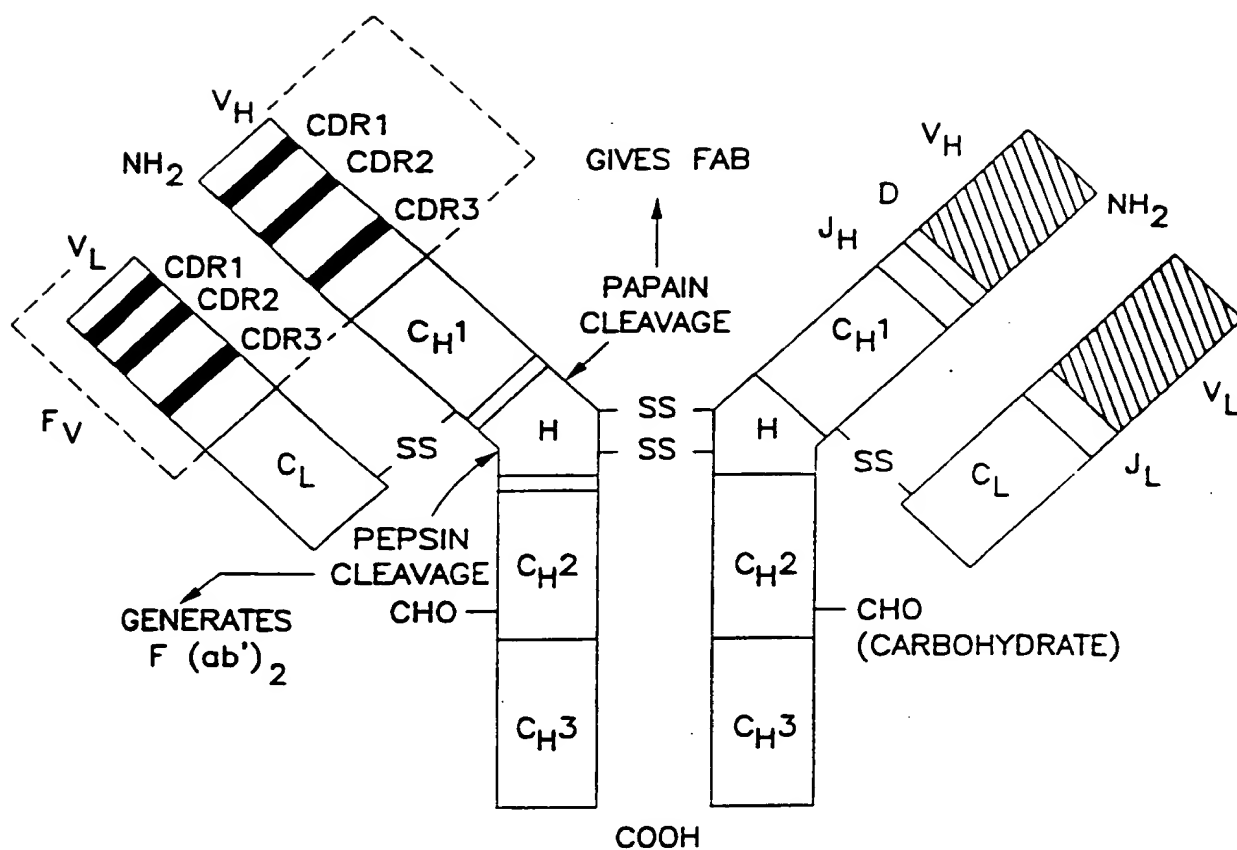


FIG. 1



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FIG. 2

Light chain

CDR 1
HuCC49
LEN
24 Lys 25 Ser 26 Ser 27 Gln 28 Asn 29 Gln 30 Lys 31 Asn 32 Tyr 33 Leu 34 Ala

CDR 2
HuCC49
LEN
50 Trp 51 Ala 52 Ser 53 Ala 54 Arg 55 Glu 56 Ser

CDR 3
HuCC49
LEN
89 Gln 90 Gln 91 Tyr 92 Tyr 93 Ser 94 Tyr 95 Pro 96 Leu 97 Thr

Heavy chain

CDR 1
HuCC49
21/28'CL
31 Asp 32 His 33 Ala 34 Ile 35 His

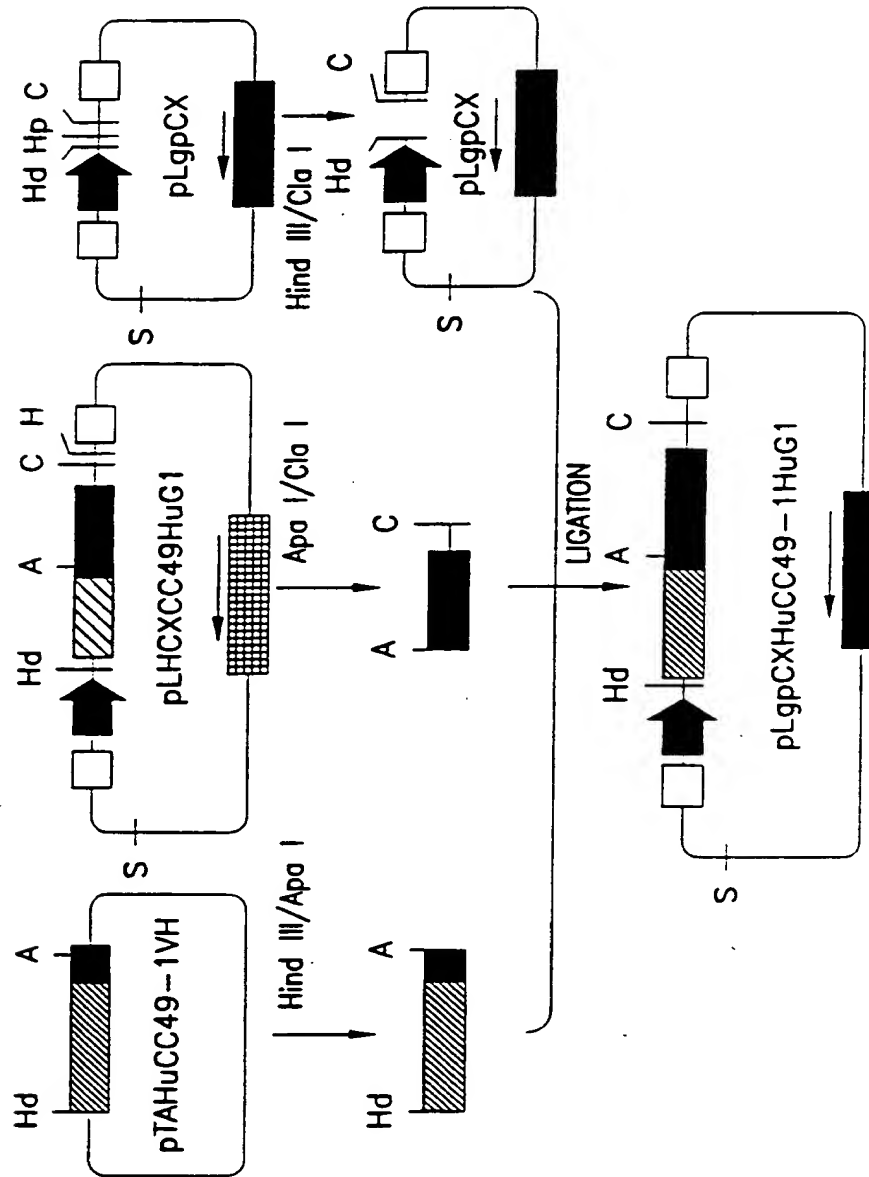
CDR 2
HuCC49
21/28'CL
50 Tyr 51 Phe 52 Ser 53 Gly 54 Asn 55 Asp 56 Asp 57 Phe 58 Lys 59 Tyr 60 Asn 61 Glu 62 Arg 63 Phe 64 Lys 65 Gly

CDR 3
HuCC49
21/28'CL
95 Ser 96 Leu 97 Asn 98 Met 99 Ala 100 Ser 101 Asn 102 Tyr

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FIG. 3



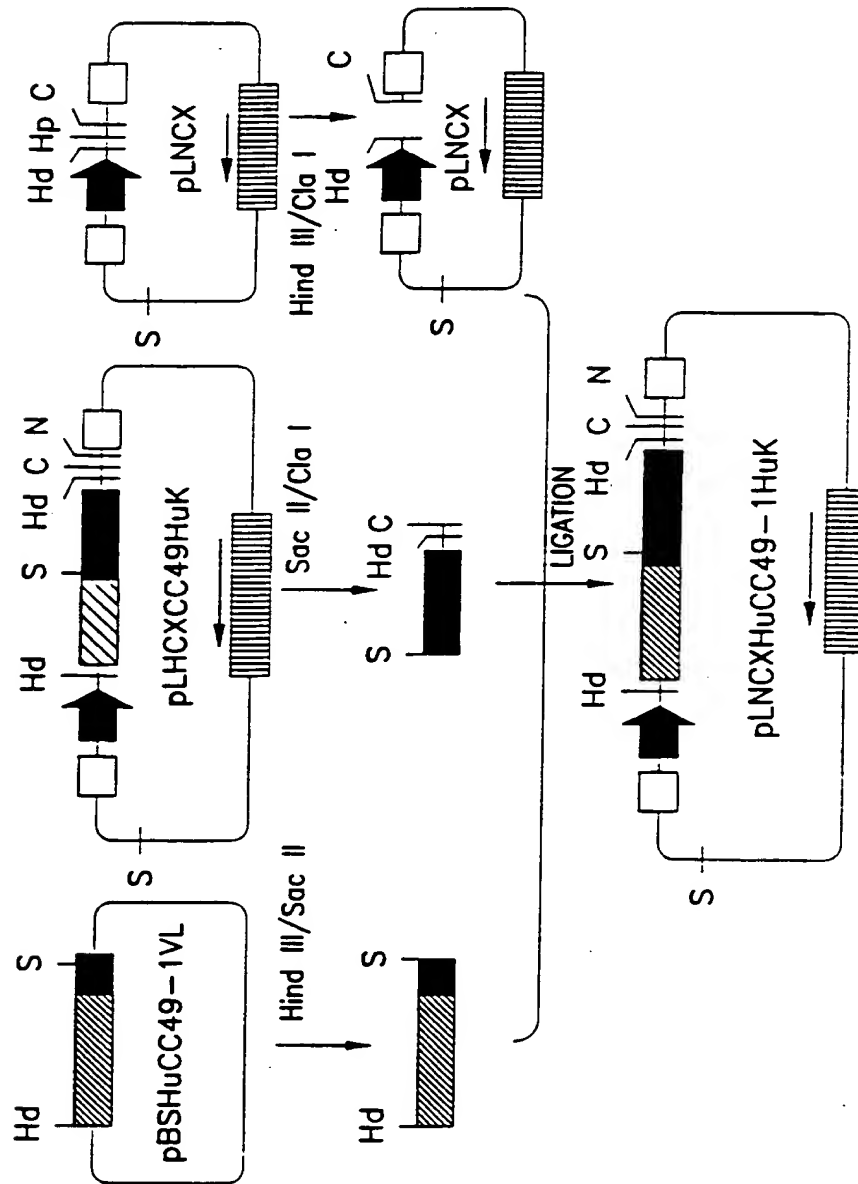
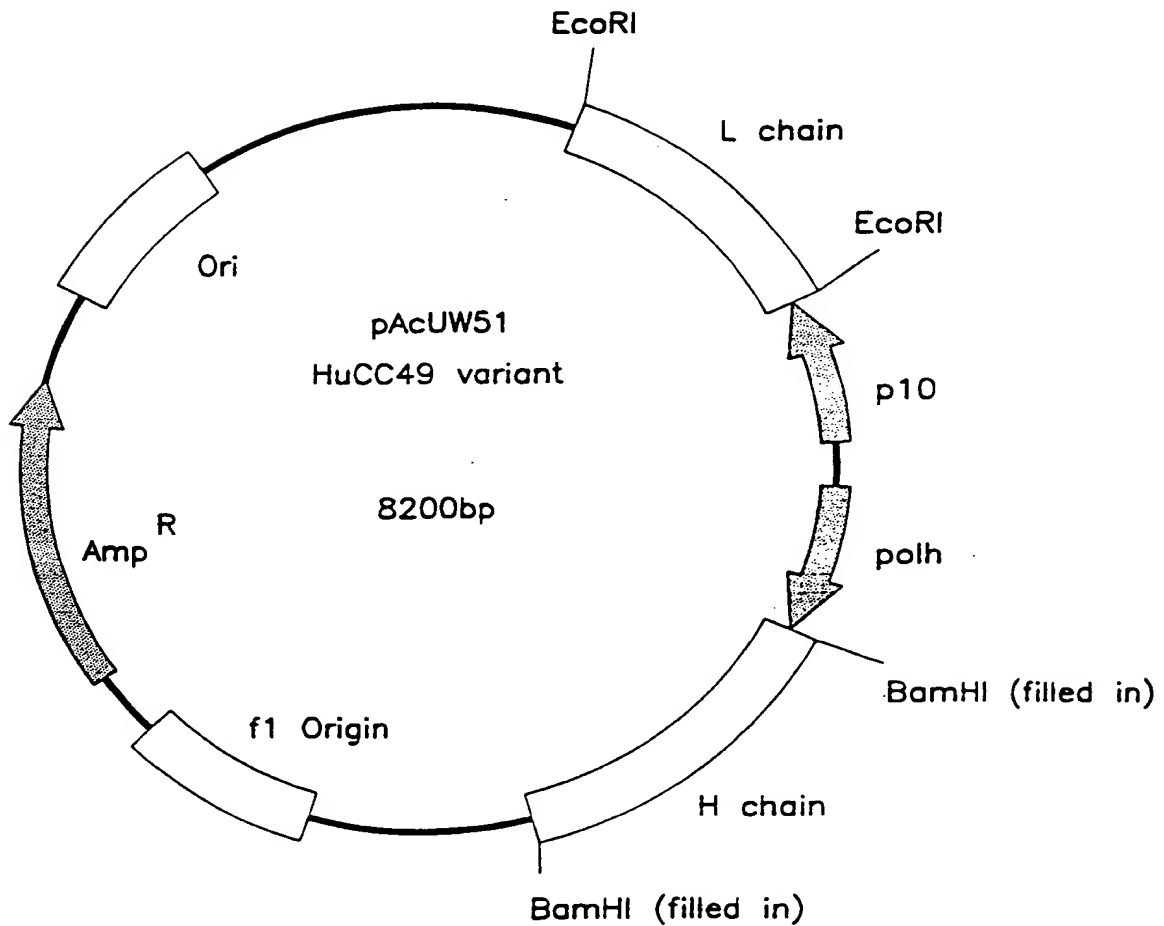


FIG. 4

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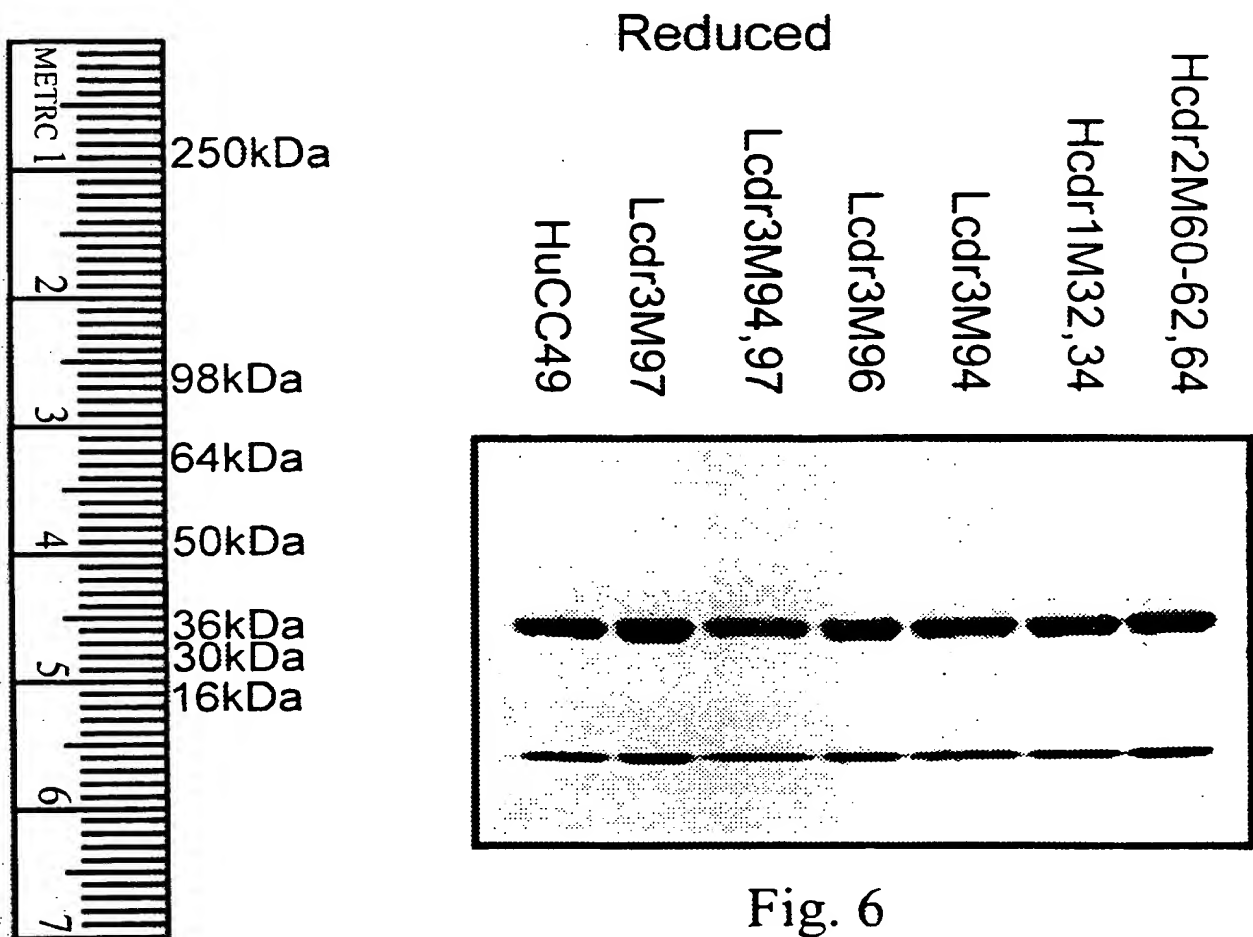
FIG. 5



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FIG. 7

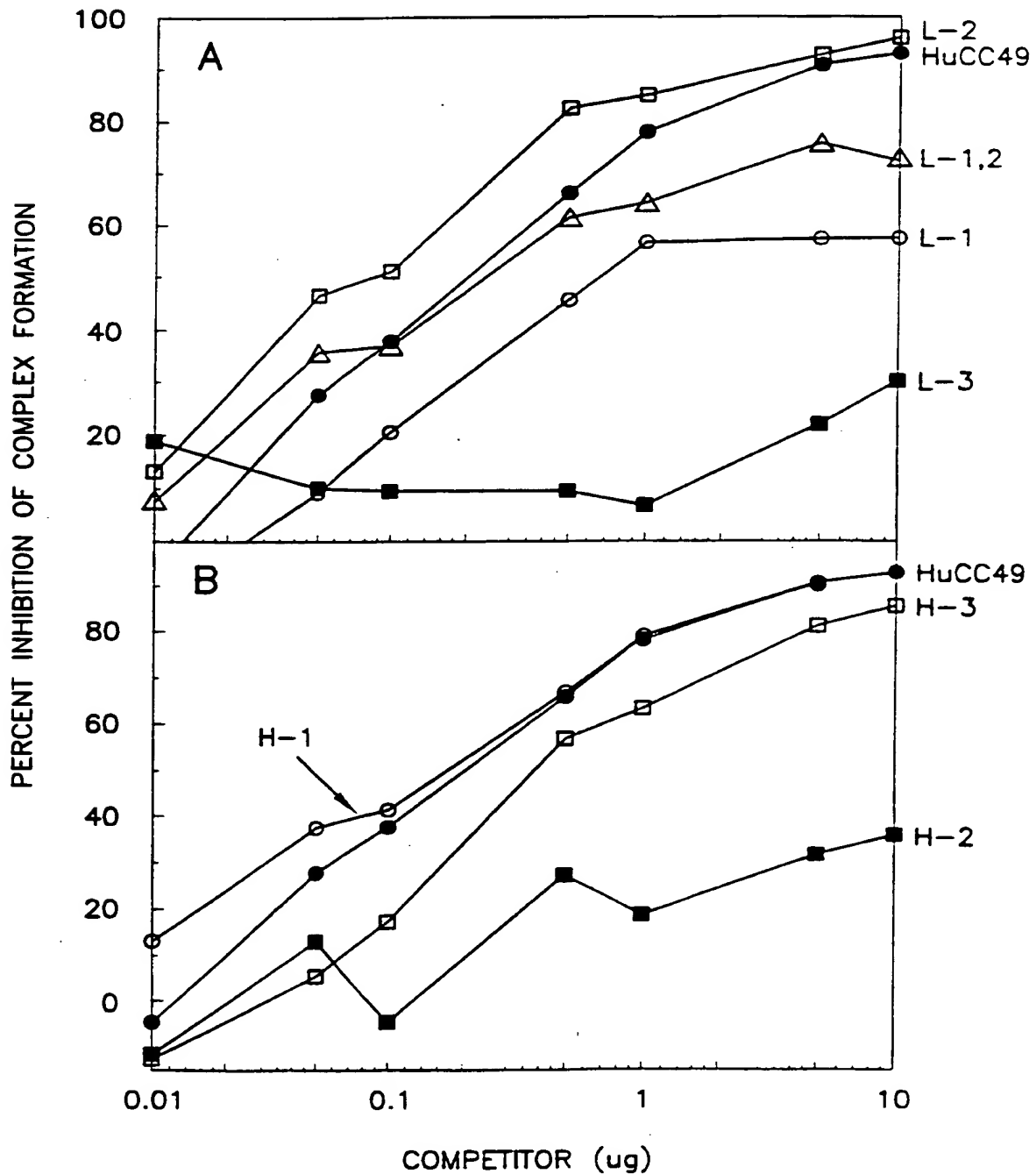
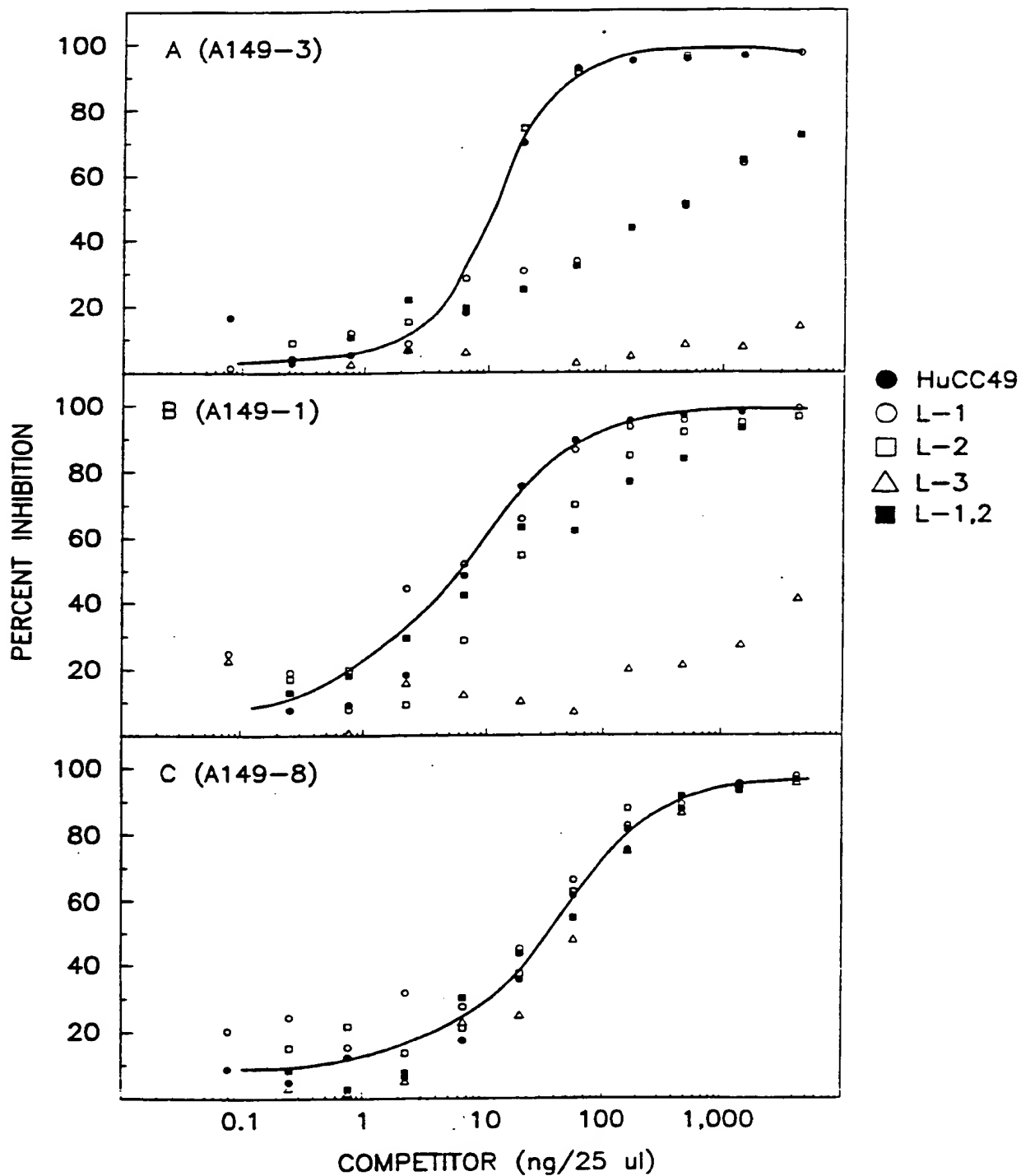


FIG. 8



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FIG. 9

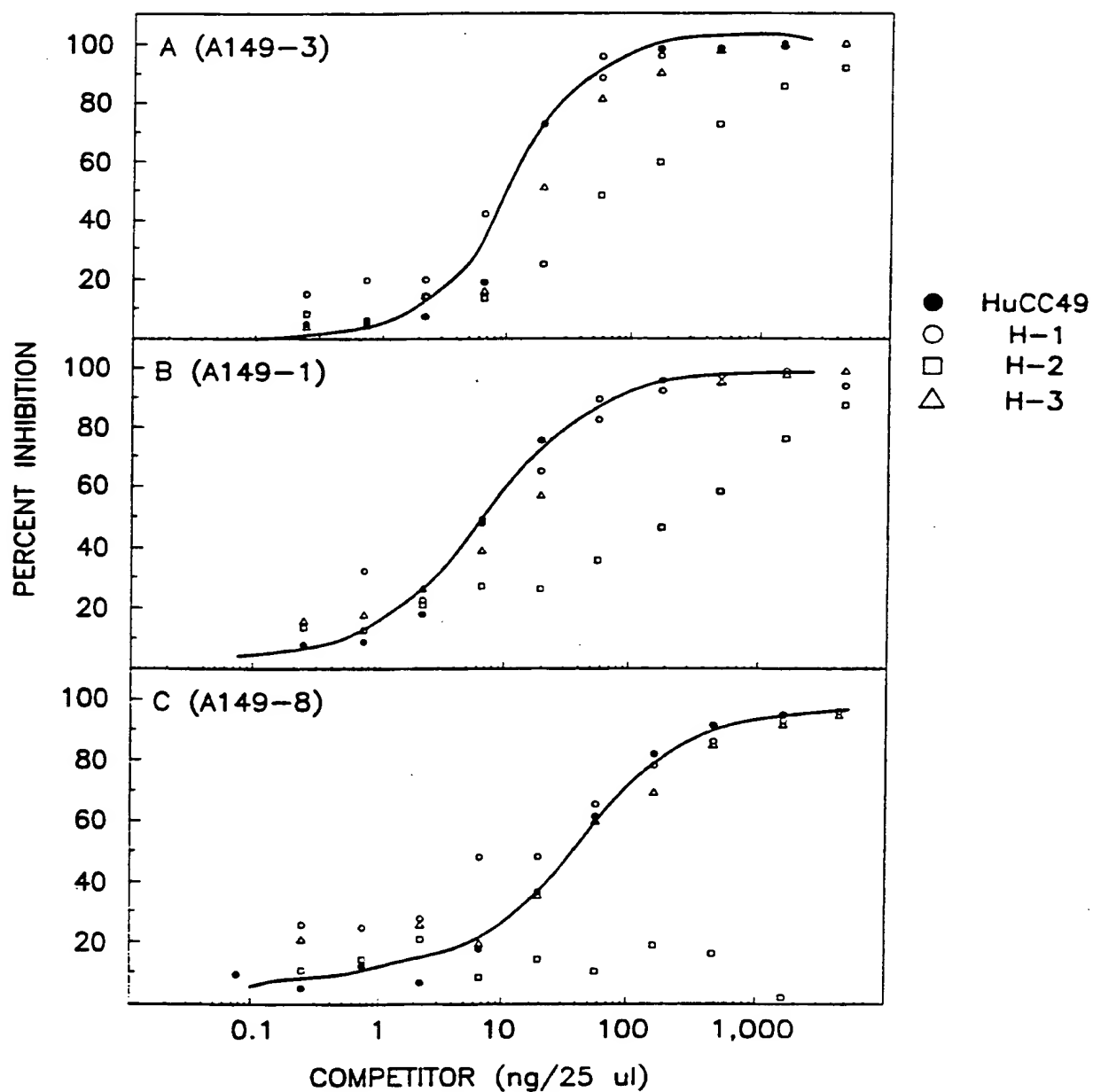


FIG. 10

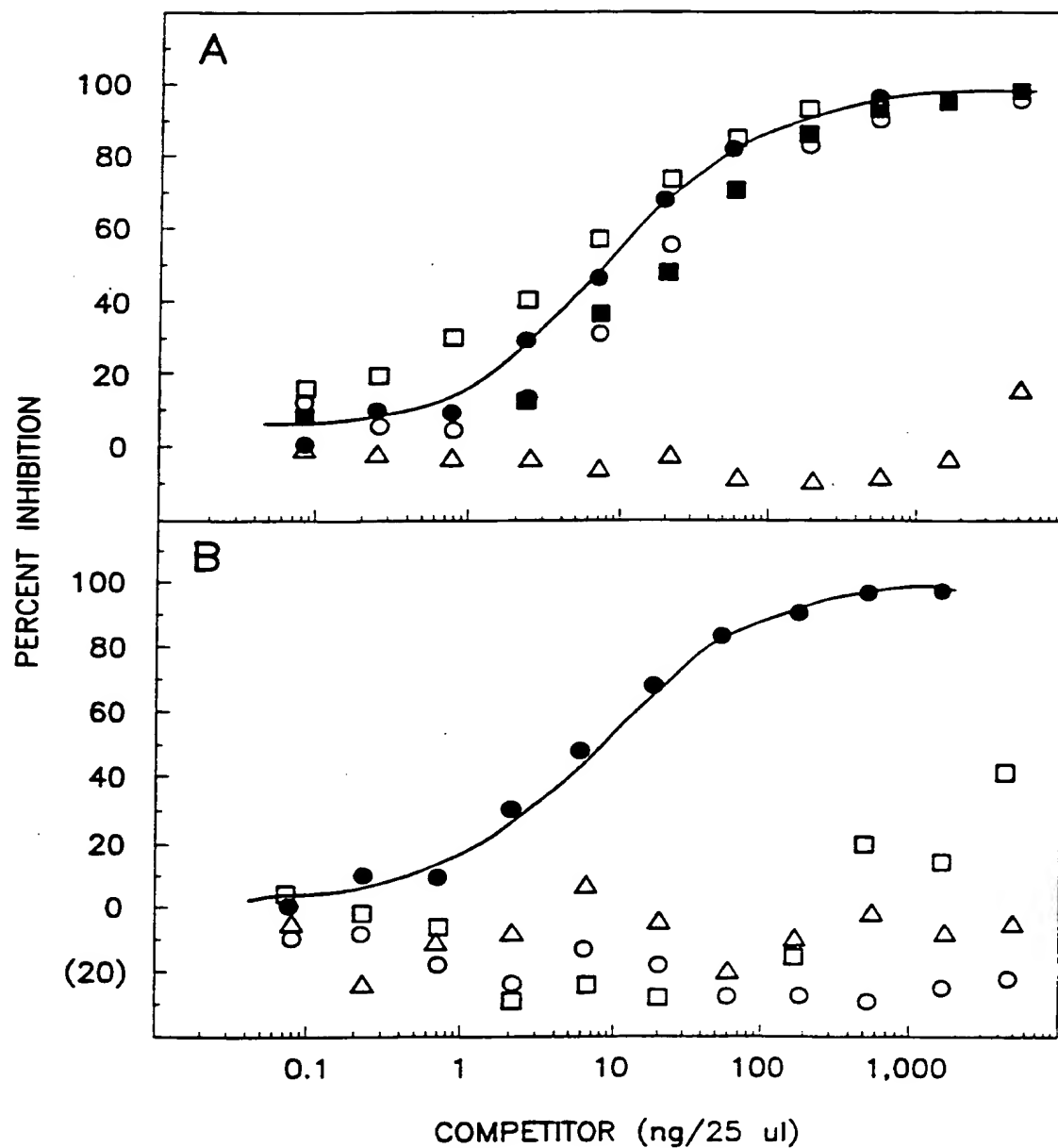


FIG. 11

A.

			CDR1		
LEN	DIVMTQSPD	SLAVSLGERATINC		WYQQKPGQPPKLLIY	
HuCC49	DIVMSQSPD	SLAVSLGERVTINC	KSSQSLLYSGNQKNYLA	WYQQKPGQSPKLLIY	
	CDR2	CDR3
LEN	WASARES	GVPDRFSGSGTDFLT	ISSLQAEDVAVYYC	FGQGTKLEIK	
HuCC49	WASARES	GVPDRFSGSGTDFLT	ISSVQAEDVAVYYC	QYYYSYPLT FGAGTKLELK	

B.

			CDR1		
21/28'CL	QVQLVQSGAEV	KKPGASVKVSKASGYTFT	WVRQAPGQRLEWMG		
HuCC49	QVQLVQSGAEV	KKPGASVKISCKASGYTFT	DHAIH WVKQNPGRLEWIG		
	CDR2
21/28'CL	YFSPGNDDFKYNERFKG	KATLTADTSASTAYVELSSLRSED	TAIVYFCAR		
HuCC49	YFSPGNDDFKYNERFKG	KATLTADTSASTAYVELSSLRSED	TAIVYFCIR		
	CDR3
21/28'CL	WGQGTLLVTVSS				
HuCC49	SLNMAY WGQGTLLVTVSS				

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FIG. 12A

 \dot{A} [illegible]

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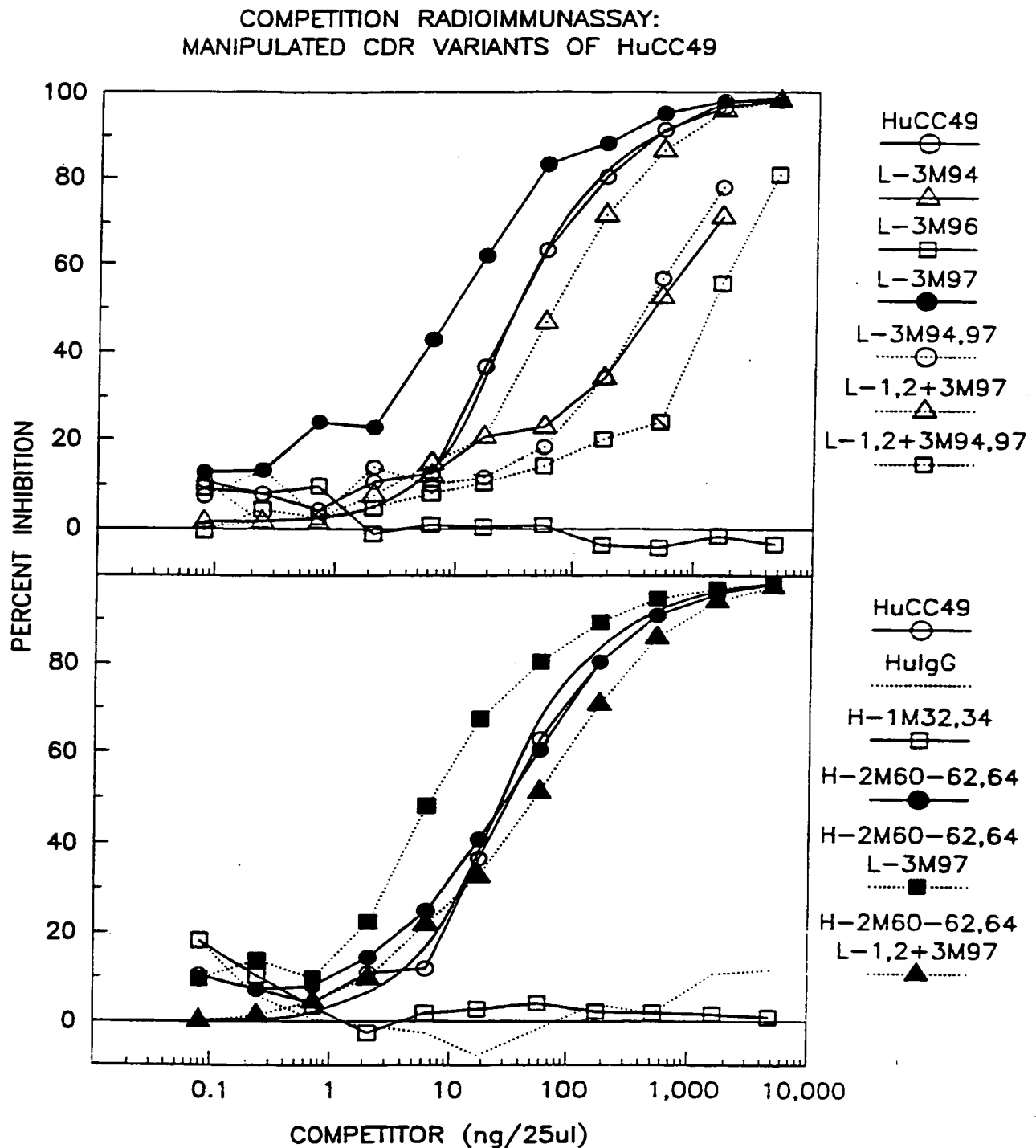
FIG. 12B

B.

```
1      c t a a g c t c c a c c a t g g a g t g g t c c t g g g t c t t c c t c t t c c t c c t g c t g c t g g g t g a g
60      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      g a t c g a a g g t g g t a c c t c a c c a g g a c c c a g a g g a g a g g a g g a c g a c a c c c a c t c
120      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      a g t g c a c t c c c a g g t c c a g c t g g t g c a g t c c g g c g c t g a g t c c c t g g c c g t g t c c c a g g g
61      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      t c a c g t g a g g t c c a g g t c g a c c a c g t c a g g c c g g a c t c a g g g a c c g g c a c a g g g a c c c
180      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      c g t g a a g a t t t c c t g c a a g g c a a g c g g c t a c a c c t t c a c t c t c t a t a g c g g a a a t c a g a a
121      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      g c a c t t c t a a a g g a c g t t c c g t t c g c c g a t g t g a a g t g a g a g a t a t c g c c t t t a g t c t t
181      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      g a a c a g a a t c c t g g a c a g c g c c t g g a g t g g a t t g g a t a t t t c t c t c c c g g a a a c g a t g a
241      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      c t t t g t c t t a g g a c c t g t c c g g a c c t c a c c t a a c c t a t a a a g a g a g g c c t t t g c t a c t
300      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      t t t t a a g t a c a a t g a g a g g t t c a a g g g c a a g g c c a c a c t g a c t g c a g a c a c a t c t g c c c a g
241      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      a a a a t t c a t g t t a c t c t c c a a g t t c c c g t t c c g g t g t g a c t g a c g t c t g t g t a g a c g g t c
360      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      c a c t g c c c t a c g t g g a g c t c t c c a g c c t g a g a t c c g a g g a t a c t g c a g t g t a c t t c t g c a c
301      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      g t g a c g g a t g c a c c t c g a g a g g t c g g a c t c t a g g c t c c t a t g a c g t c a c a t g a a g a c g t g
360      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      a a g a t c c c t g a a t a t g g c c t a c t g g g g a c a g g g a a c c c t g g t c a c c g t c t c c a g c g c c a a
361      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      t t c t a g g g a c t t a t a c c g g a t g a c c c c t g t c c c t t g g g a c c a g t g g c a g a g g t c g c g g t t
420      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      a a c t a c g g g c c c a t
434      +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      t t g a t g c c c c g g g t a
```

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FIG. 13



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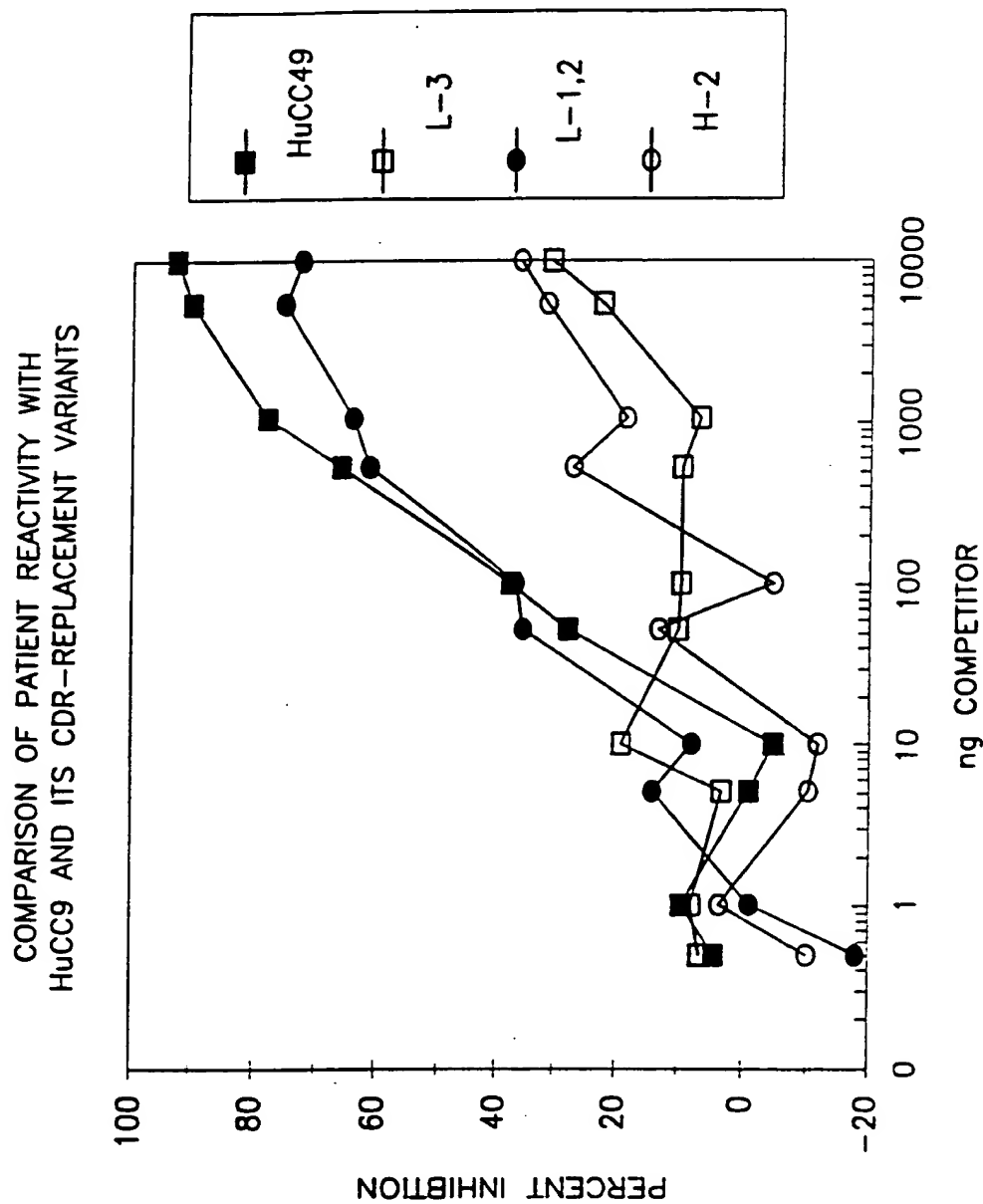
FIG. 14

HPLC ANALYSIS OF PATIENT REACTIVITY TO CDR SUBSTITUTION
VARIANTS OF HuCC49

COMPETITOR		ANTIGEN BINDING	PATIENTS			
	CDR SUBSTITUTIONS		DG	CP	EA	DS
NONE	---		46.2 ^b	32.2	56.8	33.5
HuCC49	---	+++	0	1.5	0.5	0
HuIgG	---	-	59.0	N.D.	63.6	46.4
LIGHT	L3M94	+/-	30.2	20.3	16.4	28.9
	L3M96	-	39.2	31.1	42.9	35.2
	L3M97	+++	0.6	1.3	0.7	2.4
	L3M94,97	+/-	26.5	18.2	18.6	25.6
	L1,2+3M97	++	21.3	17.6	23.8	17.1
	L1,2+3M94,97	+	53.2	38.1	44.2	37.3
HEAVY	1M32,34	-	1.4	5.5	3.8	0.7
	2M60-62,64	++	24.4	17.9	21.8	16.5
BOTH	L3M97	++++	13.0	16.1	3.9	20.1
	H2M60-62,64					
	L1,2+3M97	++	33.0	30.7	24.9	32.1
	H2M60-62,64					

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FIG. 15



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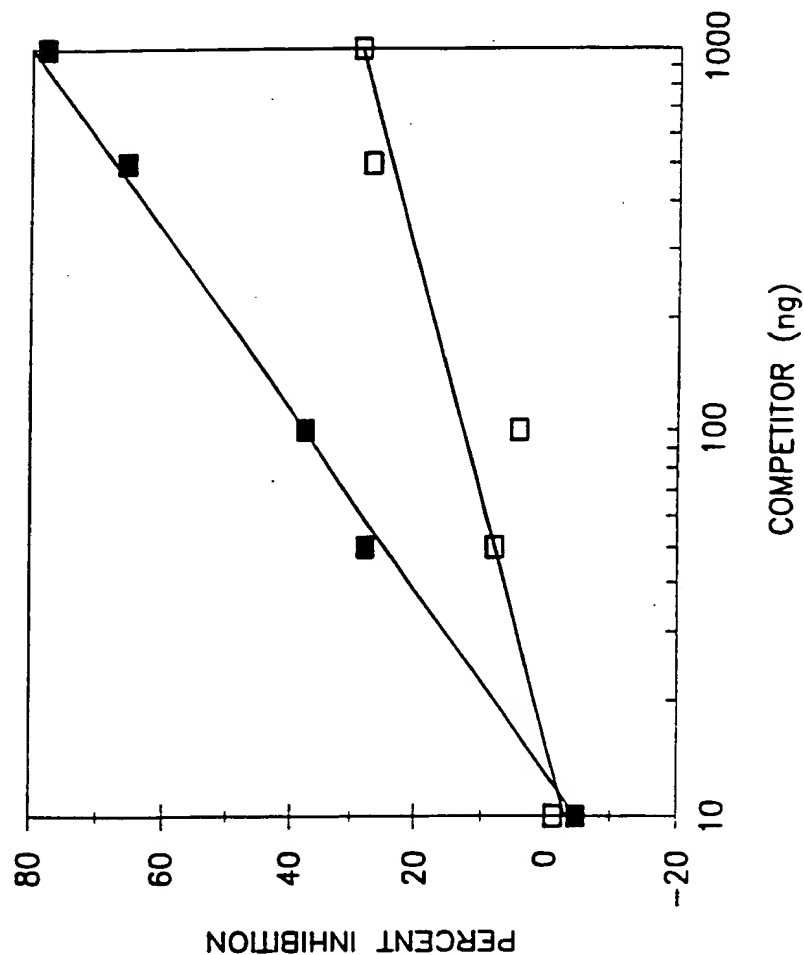


FIG. 16

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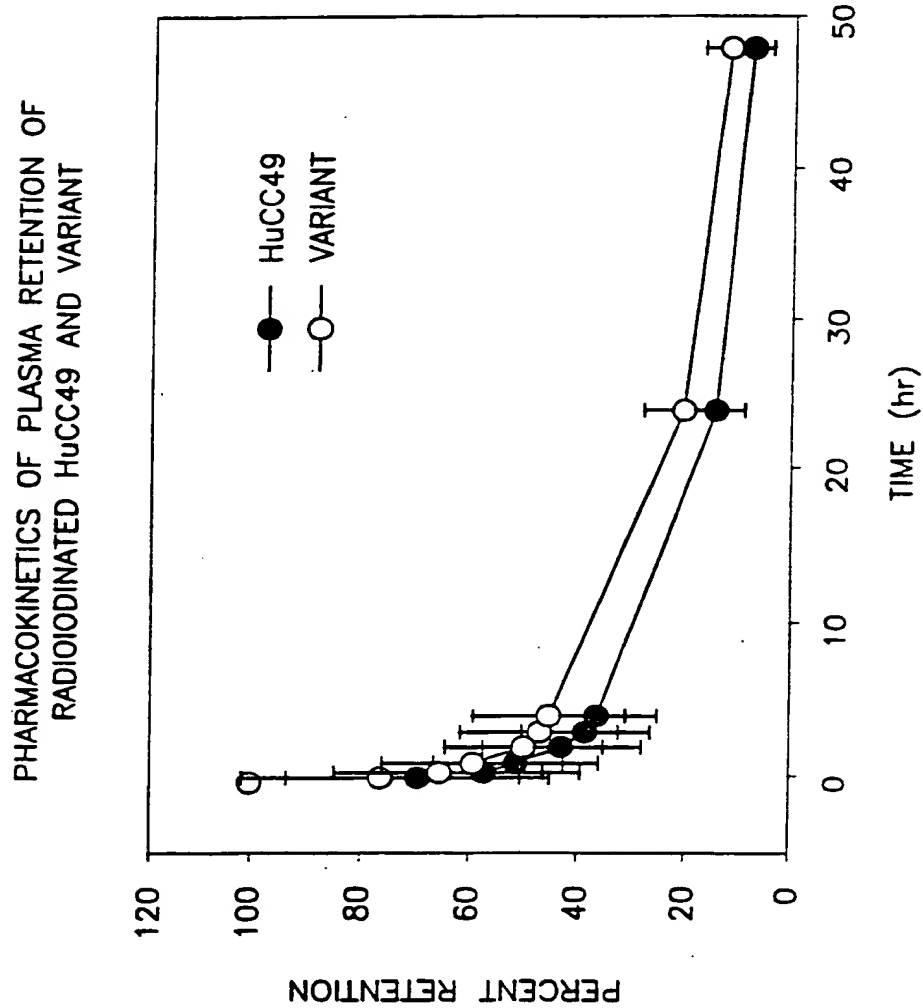


FIG. 17

FIG. 18

BIODISTRIBUTION OF I.V. ADMINISTERED RADIOLABELED HuCC49 AND VARIANT IN ATHYMIC MICE BEARING LS-174T HUMAN COLON CARCINOMA XENOGRAFTS: PERCENT OF INJECTED DOSE/GRAM

ANTIBODY	ORGAN	TIMEPOINTS (hr)				
		24	48	72	120	168
VARIANT	TUMOR	15.83	23.75	21.01	17.74	9.21
	BLOOD	6.35	4.93	4.88	2.19	0.63
	LIVER	3.39	2.14	1.46	0.91	0.32
	SPLEEN	5.90	6.04	2.55	2.43	3.96
	KIDNEY	2.52	1.27	1.00	0.77	0.36
	LUNG	3.22	2.57	2.50	1.12	0.36
HuCC49	TUMOR	11.86	17.59	15.31	13.75	5.24
	BLOOD	4.17	2.94	2.85	1.29	0.18
	LIVER	4.77	3.05	1.41	0.70	0.12
	SPLEEN	6.41	7.47	2.28	2.00	0.46
	KIDNEY	1.86	0.92	0.70	0.57	0.14
	LUNG	2.17	1.58	1.46	0.68	0.12

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FIG. 19

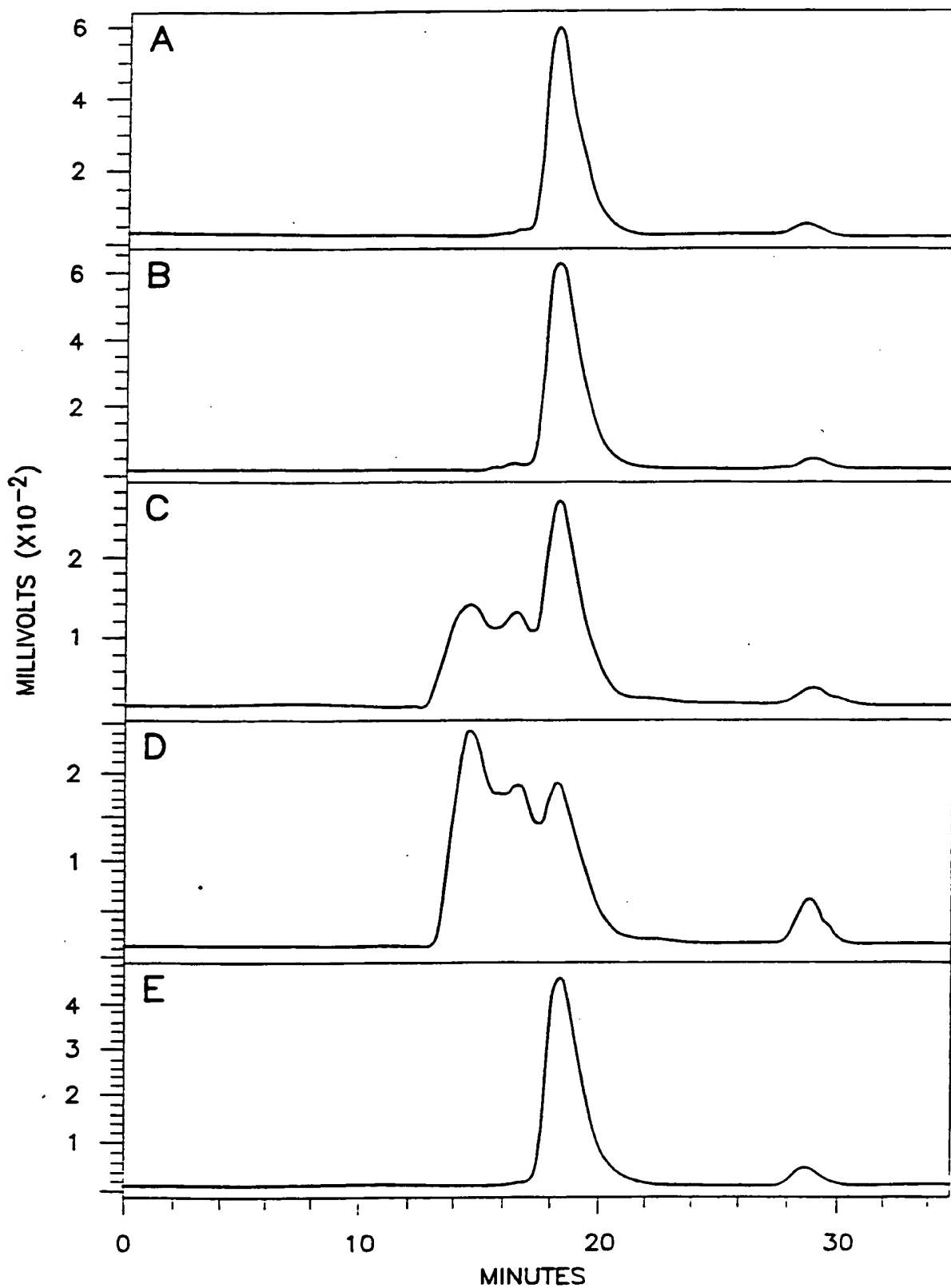


FIG. 20

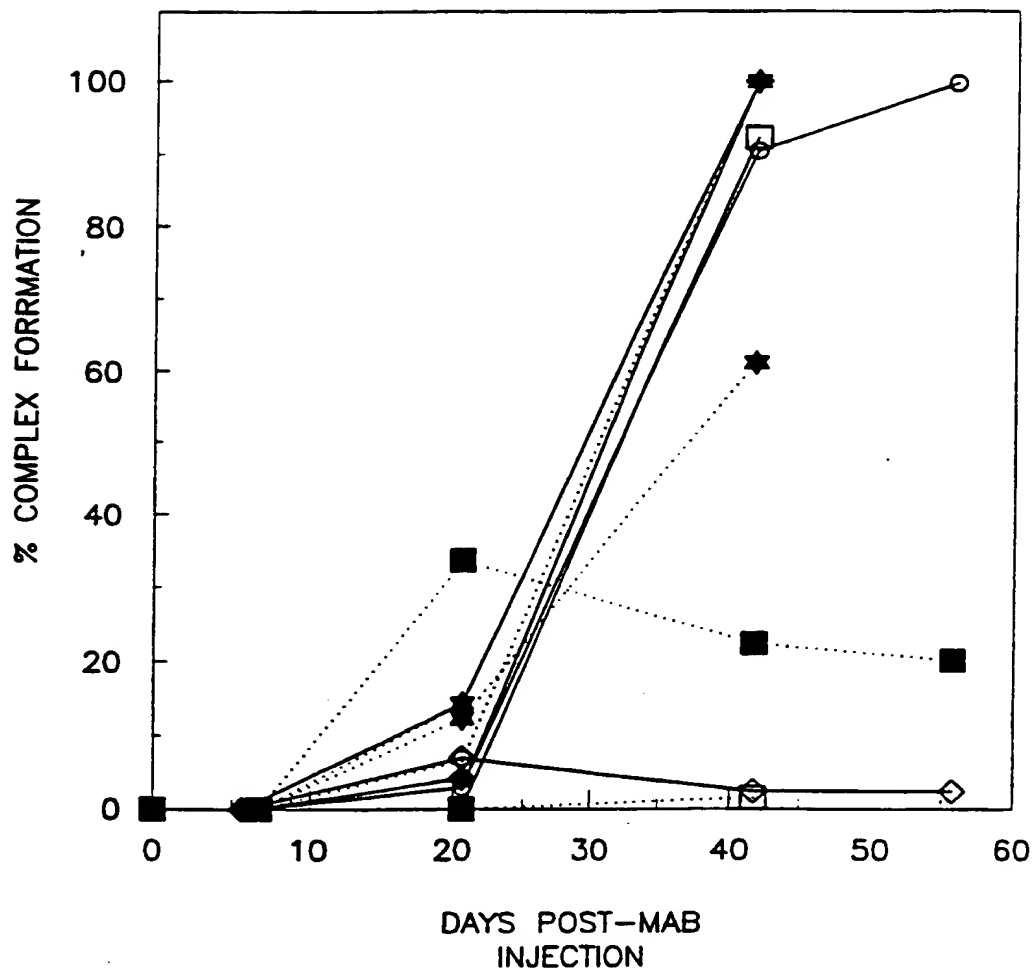
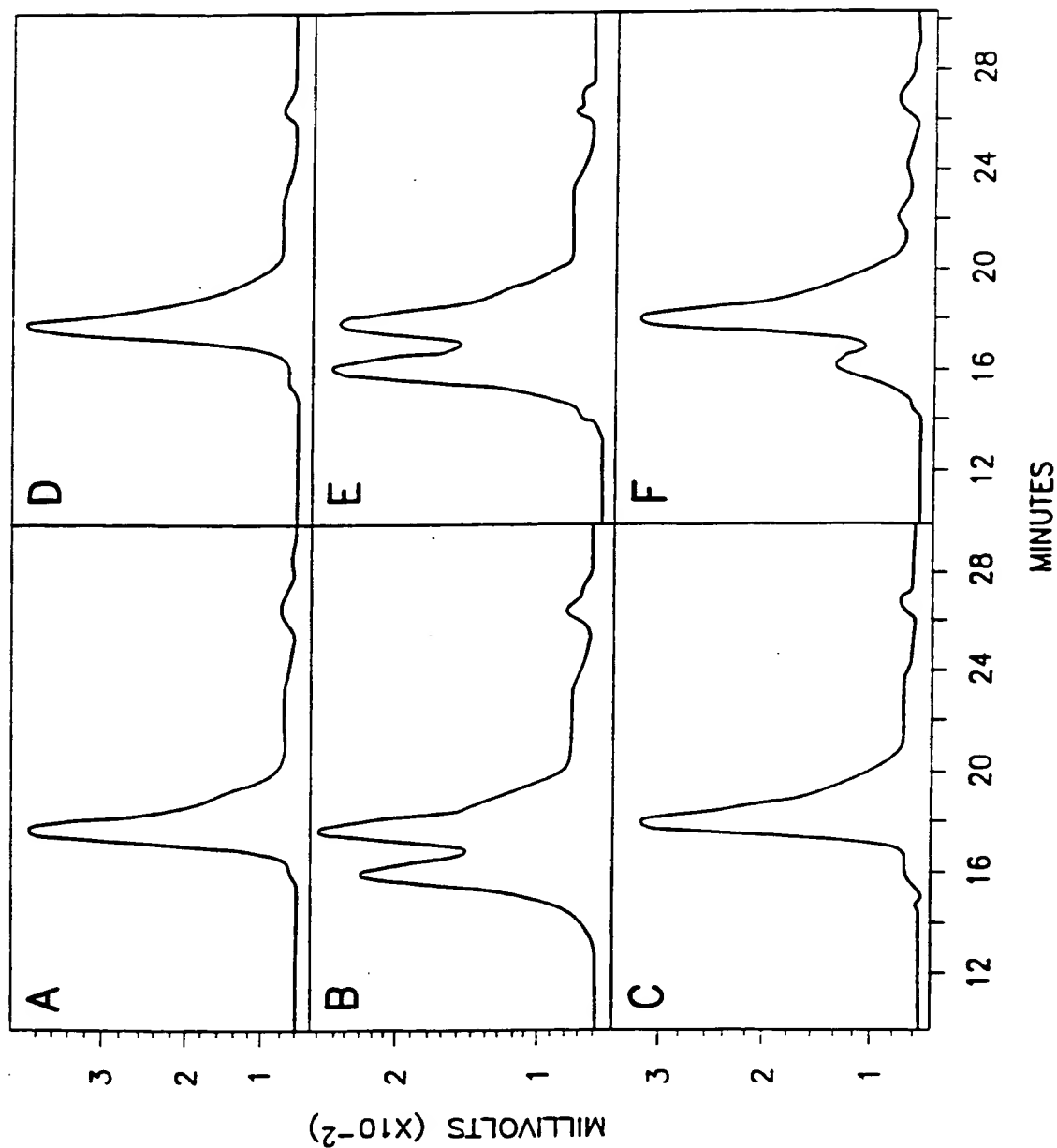


FIG. 21



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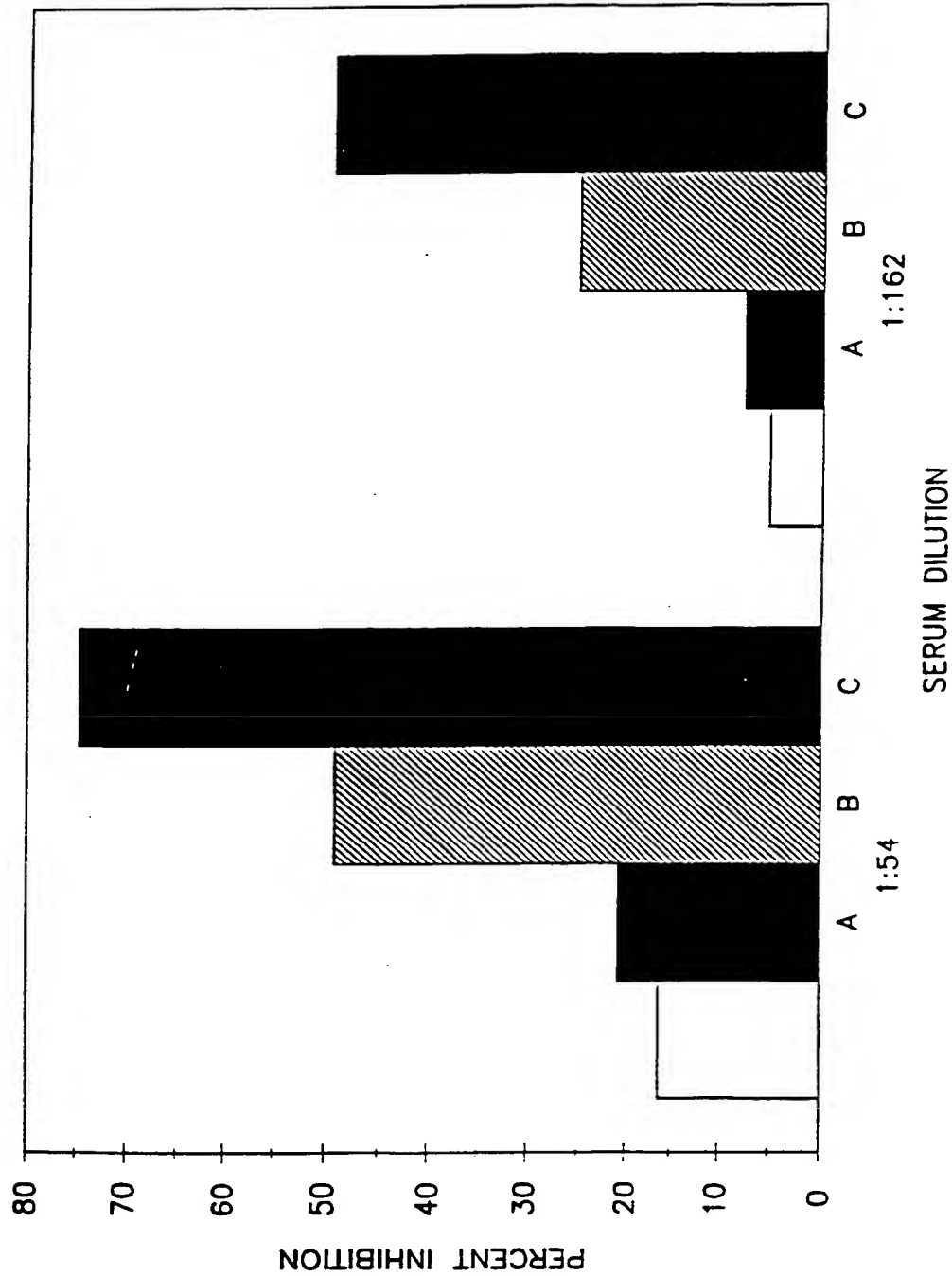


FIG. 22